RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH
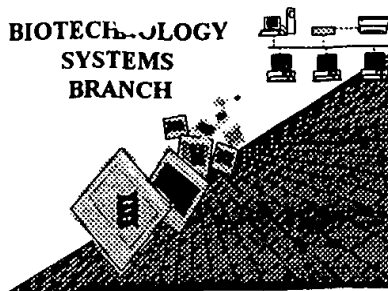
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: ___09/262,126ß___

Source: ___1600 RUSH___

Date Processed by STIC: ___2/22/2001___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/262,126B

DATE: 02/22/2001
TIME: 12:09:01

pp 1-2, 5

**Does Not Comply
Corrected Diskette Needed**

Input Set : A:\GC396-2 seq.txt
Output Set: N:\CRF3\02222001\I262126B.raw

*same error as
previous submission*

```
 3  <110> APPLICANT: Miller, Brian S.
 4        Shetty, Jayarama K.
 6  <120> TITLE OF INVENTION: Modified Forms of Pullulanase
 9  <130> FILE REFERENCE: GC396-2
11  <140> CURRENT APPLICATION NUMBER: 09/262,126B
12  <141> CURRENT FILING DATE: 1999-03-03
14  <160> NUMBER OF SEQ ID NOS: 9
16  <170> SOFTWARE: FastSEQ for Windows Version 3.0
18  <210> SEQ ID NO: 1
19  <211> LENGTH: 2794
20  <212> TYPE: DNA
21  <213> ORGANISM: B. deramificans      ──→  <220>  ←─ insert this MANDATORY
23  <221> NAME/KEY: misc_feature                numeric identifier
24  <222> LOCATION: (1)...(2794)                wherever
25  <223> OTHER INFORMATION: n = A, T, C, or G
27  <400> SEQUENCE: 1                           <221>, <222>,
28  gatgggaaca cgacaacgat cattgtccac tattttttgcc ctgctggtga ttatcaacct    60   or <223> is
29  tggagtctat ggatgtggcc aaaagacgga ggtggggctg aatacgattt caatcaaccg   120   shown.
30  gctgactctt ttggagctgt tgcaagtgct gatattccag gaaacccaag tcaggtagga   180
31  attatcgttc gcactcaaga ttggaccaaa gatgtgagcg ctgaccgcta catagattta   240
32  agcaaaggaa atgaggtgtg gcttgtagaa ggaaacagcc aaatttttta taatgaaaaa   300
33  gatgctgagg atgcagctaa acccgctgta agcaacgctt atttagatgc ttcaaaccag   360
34  gtgctggtta aacttagcca gccgttaact cttggggaag gnnnaagcgg ctttacggtt   420
35  catgacgaca cagcaaataa ggatattcca gtgacatctg tgaaggatgc aagtcttggt   480
36  caagatgtaa ccgctgtttt ggcaggtacc ttccaacata ttttttggagg ttccgattgg   540
37  gcacctgata atcacagtac tttattaaaa aaggtgacta acaatctcta tcaattctca   600
38  ggagatcttc ctgaaggaaa ctaccaatat aaagtggctt aaatgatag ctggaataat   660
39  ccgagttacc catctgacaa cattaattta acagtccctg ccggcggtgc acacgtcact   720
40  tttttcgtata ttccgtccac tcatgcagtc tatgacacaa ttaataatcc taatgcggat   780
41  ttacaagtag aaagcggggt taaaacggat ctcgtgacgg ttactctagg ggaagatcca   840
42  gatgtgagcc atactctgtc cattcaaaca gatggctatc aggcaaagca ggtgatacct   900
43  cgtaatgtgc ttaattcatc acagtactac tattcaggag atgatcttgg gaatacctat   960
44  acacagaaag caacaacctt taaagtctgg gcaccaactt ctactcaagt aaatgttctt  1020
45  ctttatgaca gtgcaacggg ttctgtaaca aaaatcgtac ctatgacggc atcgggccat  1080
46  ggtgtgtggg aagcaacggt taatcaaaac cttgaaaatt ggtattacat gtatgaggta  1140
47  acaggccaag gctctacccg aacggctgtt gatccttatg caactgcgat tgcaccaaat  1200
48  ggaacgagag gcatgattgt ggacctggct aaaacagatc ctgctggctg gaacagtgat  1260
49  aaacatatta cgccaaagaa tatagaagat gaggtcatct atgaaatgga tgtccgtgac  1320
50  ttttccattg accctaattc gggtatgaaa aataaaggga agtatttggc tcttacagaa  1380
51  aaaggaacaa agggccctga caacgtaaag acggggatag attccttaaa acaacttggg  1440
52  attactcatg ttcagcttat gcctgttttc gcatctaaca gtgtcgatga aactgatcca  1500
53  acccaagata attggggtta tgaccctcgc aactatgatg ttcctgaagg gcagtatgct  1560
54  acaaatgcga atggtaatgc tcgtataaaa gagtttaagg aaatggttct ttcactccat  1620
55  cgtgaacaca ttggggggttaa catggatgtt gtctataatc ataccttgc cacgcaaatc  1680
56  tctgacttcg ataaaaattgt accagaatat tattaccgta cgatgatcca ggtaattata  1740
57  ccaacggatc aggtactgga aatgaaattg cangcngaaa ggccaatggt tcaaaaattt  1800
58  attattgatt cccttaagta ttgggtcaat gagtatcata ttgacggctt ccgttttgac  1860
```

RAW SEQUENCE LISTING   DATE: 02/22/2001
PATENT APPLICATION: US/09/262,126B   TIME: 12:09:01

Input Set : A:\GC396-2 seq.txt
Output Set: N:\CRF3\02222001\I262126B.raw

```
59  ttaatggcgc tgcttggaaa agacacgatg tccaaagctg cctcggagct tcatgctatt    1920
60  aatccaggaa ttgcacttta cggtgagcca tggacgggtg gaacctctgc actgccagat    1980
61  gatcagcttc tgacaaaagg agctcaaaaa ggcatgggag tagcggtgtt taatgacaat    2040
62  ttacgaaacg cgttggacgg caatgtcttt gattcttccg ctcaaggttt tgcgacaggt    2100
63  gcaacaggct taactgatgc aattaagaat ggcgttgagg ggagtattaa tgactttacc    2160
64  tcttcaccag gtgagacaat taactatgtc acaagtcatg ataactacac cctttgggac    2220
65  aaaatagccc taagcaatcc taatgattcc gaagcggatc ggattaaaat ggatgaactc    2280
66  gcacaagcag ttgttatgac ctcacaaggc gttccattca tgcaaggcgg ggaagaaatg    2340
67  cttcgtanaa aaggcggcaa cgacaatagt tataatgcag gcgatgcggt caatgagttt    2400
68  gattggagca ggaaagctca atatccagat gtttttcaact attatagcgg gctaatccac    2460
69  cttcgtcttg atcacccagc cttccgcatg acgacagcta atgaaatcaa tagccacctc    2520
70  caattcctaa atagtccaga gaacacagtg gcctatgaat taactgatca tgttaataaa    2580
71  gacaaatggg gaaatatcat tgttgtttat aacccaaata aaactgtagc aaccatcaat    2640
72  ttgccgagcg gyaaatgggc aatcaatgct acgagcggta aggtaggaga atccaccctt    2700
73  ggtcaagcag agggaagtgt ccaagtacca ggtatatcta tgatgatcct tcatcaagag    2760
74  gtaagcccag accacggtaa aaagtaatag aaaa                                 2794
76  <210> SEQ ID NO: 2
77  <211> LENGTH: 958
78  <212> TYPE: PRT
79  <213> ORGANISM: B. deramificans
81  <220> FEATURE:
82  <221> NAME/KEY: VARIANT
83  <222> LOCATION: (1)...(956)
84  <223> OTHER INFORMATION: Xaa = Any Amino Acid
86  <220> FEATURE:
87  <221> NAME/KEY: VARIANT
88  <222> LOCATION: (957)...(957)
89  <223> OTHER INFORMATION: Xaa = gap of indeterminate length
91  <400> SEQUENCE: 2
92  Met Ala Lys Lys Leu Ile Tyr Val Cys Leu Ser Val Cys Leu Val Leu
93   1               5                  10                  15
94  Thr Trp Ala Phe Asn Val Lys Gly Gln Ser Ala His Ala Asp Gly Asn
95              20                  25                  30
96  Thr Thr Thr Ile Ile Val His Tyr Phe Cys Pro Ala Gly Asp Tyr Gln
97              35                  40                  45
98  Pro Trp Ser Leu Trp Met Trp Pro Lys Asp Gly Gly Gly Ala Glu Tyr
99      50                  55                  60
100 Asp Phe Asn Gln Pro Ala Asp Ser Phe Gly Ala Val Ala Ser Ala Asp
101 65                  70                  75                  80
102 Ile Pro Gly Asn Pro Ser Gln Val Gly Ile Ile Val Arg Thr Gln Asp
103              85                  90                  95
104 Trp Thr Lys Asp Val Ser Ala Asp Arg Tyr Ile Asp Leu Ser Lys Gly
105             100                 105                 110
106 Asn Glu Val Trp Leu Val Glu Gly Asn Ser Gln Ile Phe Tyr Asn Glu
107             115                 120                 125
108 Lys Asp Ala Glu Asp Ala Ala Lys Pro Ala Val Ser Asn Ala Tyr Leu
109     130                 135                 140
110 Asp Ala Ser Asn Gln Val Leu Val Lys Leu Ser Gln Pro Leu Thr Leu
111 145                 150                 155                 160
```

invalid

[handwritten right margin:]
Xaa can only represent a single amino acid.

Per 1.822(d)(5)(e) of new Sequence Rules, "A sequence with a gap or gaps shall be presented as a plurality of separate sequences..."

However, since only one amino acid follows gap, and at least four amino acids are needed for a sequence, delete last amino acid and adjust <211> response to 957

file://C:\Crf3\Outhold\VsrI262126B.htm

```
W--> 112   Gly Glu Gly Xaa Ser Gly Phe Thr Val His Asp Asp Thr Ala Asn Lys
     113               165             170             175
     114   Asp Ile Pro Val Thr Ser Val Lys Asp Ala Ser Leu Gly Gln Asp Val
     115               180             185             190
     116   Thr Ala Val Leu Ala Gly Thr Phe Gln His Ile Phe Gly Gly Ser Asp
     117               195             200             205
     118   Trp Ala Pro Asp Asn His Ser Thr Leu Leu Lys Lys Val Thr Asn Asn
     119       210             215             220
     120   Leu Tyr Gln Phe Ser Gly Asp Leu Pro Glu Gly Asn Tyr Gln Tyr Lys
     121   225             230             235                         240
     122   Val Ala Leu Asn Asp Ser Trp Asn Asn Ser Tyr Pro Ser Asp Asn Ile
     123               245             250             255
     124   Asn Leu Thr Val Pro Ala Gly Gly Ala His Val Thr Phe Ser Tyr Ile
     125               260             265             270
     126   Pro Ser Thr His Ala Val Tyr Asp Thr Ile Asn Asn Pro Asn Ala Asp
     127               275             280             285
     128   Leu Gln Val Glu Ser Gly Val Lys Thr Asp Leu Val Thr Val Thr Leu
     129       290             295             300
     130   Gly Glu Asp Pro Asp Val Ser His Thr Leu Ser Ile Gln Thr Asp Gly
     131   305             310             315                         320
     132   Tyr Gln Ala Lys Gln Val Ile Pro Arg Asn Val Leu Asn Ser Ser Gln
     133               325             330             335
     134   Tyr Tyr Tyr Ser Gly Asp Asp Leu Gly Asn Thr Tyr Thr Gln Lys Ala
     135               340             345             350
     136   Thr Thr Phe Lys Val Trp Ala Pro Thr Ser Thr Gln Val Asn Val Leu
     137               355             360             365
     138   Leu Tyr Asp Ser Ala Thr Gly Ser Val Thr Lys Ile Val Pro Met Thr
     139       370             375             380
     140   Ala Ser Gly His Gly Val Trp Glu Ala Thr Val Asn Gln Asn Leu Glu
     141   385             390             395                         400
     142   Asn Trp Tyr Tyr Met Tyr Glu Val Thr Gly Gln Gly Ser Thr Arg Thr
     143               405             410             415
     144   Ala Val Asp Pro Tyr Ala Thr Ala Ile Ala Pro Asn Gly Thr Arg Gly
     145               420             425             430
     146   Met Ile Val Asp Leu Ala Lys Thr Asp Pro Ala Gly Trp Asn Ser Asp
     147               435             440             445
     148   Lys His Ile Thr Pro Lys Asn Ile Glu Asp Glu Val Ile Tyr Glu Met
     149       450             455             460
     150   Asp Val Arg Asp Phe Ser Ile Asp Pro Asn Ser Gly Met Lys Asn Lys
     151   465             470             475                         480
     152   Gly Lys Tyr Leu Ala Leu Thr Glu Lys Gly Thr Lys Gly Pro Asp Asn
     153               485             490             495
     154   Val Lys Thr Gly Ile Asp Ser Leu Lys Gln Leu Gly Ile Thr His Val
     155               500             505             510
     156   Gln Leu Met Pro Val Phe Ala Ser Asn Ser Val Asp Glu Thr Asp Pro
     157               515             520             525
     158   Thr Gln Asp Asn Trp Gly Tyr Asp Pro Arg Asn Tyr Asp Val Pro Glu
     159       530             535             540
     160   Gly Gln Tyr Ala Thr Asn Ala Asn Gly Asn Ala Arg Ile Lys Glu Phe
```

RAW SEQUENCE LISTING   DATE: 02/22/2001
PATENT APPLICATION: US/09/262,126B   TIME: 12:09:01

Input Set : A:\GC396-2 seq.txt
Output Set: N:\CRF3\02222001\I262126B.raw

```
      161 545                  550                  555                  560
      162 Lys Glu Met Val Leu Ser Leu His Arg Glu His Ile Gly Val Asn Met
      163                  565                  570                  575
      164 Asp Val Val Tyr Asn His Thr Phe Ala Thr Gln Ile Ser Asp Phe Asp
      165                  580                  585                  590
      166 Lys Ile Val Pro Glu Tyr Tyr Tyr Arg Thr Met Ile Gln Val Ile Ile
      167                  595                  600                  605
W--> 168 Pro Thr Asp Gln Val Leu Glu Met Lys Leu Xaa Ala Glu Arg Pro Met
      169      610    .             615                  620
      170 Val Gln Lys Phe Ile Ile Asp Ser Leu Lys Tyr Trp Val Asn Glu Tyr
      171 625                  630                  635                  640
      172 His Ile Asp Gly Phe Arg Phe Asp Leu Met Ala Leu Leu Gly Lys Asp
      173                  645                  650                  655
      174 Thr Met Ser Lys Ala Ala Ser Glu Leu His Ala Ile Asn Pro Gly Ile
      175                  660                  665                  670
      176 Ala Leu Tyr Gly Glu Pro Trp Thr Gly Gly Thr Ser Ala Leu Pro Asp
      177                  675                  680                  685
      178 Asp Gln Leu Leu Thr Lys Gly Ala Gln Lys Gly Met Gly Val Ala Val
      179      690        .        695                  700
      180 Phe Asn Asp Asn Leu Arg Asn Ala Leu Asp Gly Asn Val Phe Asp Ser
      181 705                  710                  715                  720
      182 Ser Ala Gln Gly Phe Ala Thr Gly Ala Thr Gly Leu Thr Asp Ala Ile
      183                  725                  730                  735
      184 Lys Asn Gly Val Glu Gly Ser Ile Asn Asp Phe Thr Ser Ser Pro Gly
      185                  740                  745                  750
      186 Glu Thr Ile Asn Tyr Val Thr Ser His Asp Asn Tyr Thr Leu Trp Asp
      187                  755                  760                  765
      188 Lys Ile Ala Leu Ser Asn Pro Asn Asp Ser Glu Ala Asp Arg Ile Lys
      189      770                  775                  780
      190 Met Asp Glu Leu Ala Gln Ala Val Val Met Thr Ser Gln Gly Val Pro
      191 785                  790                  795                  800
W--> 192 Phe Met Gln Gly Gly Glu Glu Met Leu Arg Xaa Lys Gly Gly Asn Asp
      193                  805                  810        .        815
      194 Asn Ser Tyr Asn Ala Gly Asp Ala Val Asn Glu Phe Asp Trp Ser Arg
      195                  820                  825                  830
      196 Lys Ala Gln Tyr Pro Asp Val Phe Asn Tyr Tyr Ser Gly Leu Ile His
      197                  835                  840                  845
      198 Leu Arg Leu Asp His Pro Ala Phe Arg Met Thr Thr Ala Asn Glu Ile
      199      850                  855                  860
      200 Asn Ser His Leu Gln Phe Leu Asn Ser Pro Glu Asn Thr Val Ala Tyr
      201 865.                 870                  875                  880
      202 Glu Leu Thr Asp His Val Asn Lys Asp Lys Trp Gly Asn Ile Ile Val
      203                  885                  890                  895
      204 Val Tyr Asn Pro Asn Lys Thr Val Ala Thr Ile Asn Leu Pro Ser Gly
      205                  900                  905                  910
      206 Lys Trp Ala Ile Asn Ala Thr Ser Gly Lys Val Gly Glu Ser Thr Leu
      207                  915                  920                  925
      208 Gly Gln Ala Glu Gly Ser Val Gln Val Pro Gly Ile Ser Met Met Ile
      209      930                  935                  940
```

```
W--> 210   Leu His Gln Glu Val Ser Pro Asp His Gly Lys Lys Xaa Lys  delete
     211   945             950             955
     213 <210> SEQ ID NO: 3
     214 <211> LENGTH: 718
     215 <212> TYPE: PRT
     216 <213> ORGANISM: B. subtilis
     218 <400> SEQUENCE: 3
     219   Met Val Ser Ile Arg Arg Ser Phe Glu Ala Tyr Val Asp Asp Met Asn
     220   1               5                   10                  15
     221   Ile Ile Thr Val Leu Ile Pro Ala Glu Gln Lys Glu Ile Met Thr Pro
     222               20                  25                  30
     223   Pro Phe Arg Leu Glu Thr Glu Ile Thr Asp Phe Pro Leu Ala Val Arg
     224               35                  40                  45
     225   Glu Glu Tyr Ser Leu Glu Ala Lys Tyr Lys Tyr Val Cys Val Ser Asp
     226       50                  55                  60
     227   His Pro Val Thr Phe Gly Lys Ile His Cys Val Arg Ala Ser Ser Gly
     228   65                  70                  75                  80
     229   His Lys Thr Asp Leu Gln Ile Gly Ala Val Ile Arg Thr Ala Ala Phe
     230               85                  90                  95
     231   Asp Asp Glu Phe Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Thr Ala
     232               100                 105                 110
     233   Asp His Thr Val Phe Lys Val Trp Ala Pro Ala Ala Thr Ser Ala Ala
     234               115                 120                 125
     235   Val Lys Leu Ser His Pro Asn Lys Ser Gly Arg Thr Phe Gln Met Thr
     236       130                 135                 140
     237   Arg Leu Glu Lys Gly Val Tyr Ala Val Thr Val Thr Gly Asp Leu His
     238   145                 150                 155                 160
     239   Gly Tyr Glu Tyr Leu Phe Cys Ile Cys Asn Asn Ser Glu Trp Met Glu
     240               165                 170                 175
     241   Thr Val Asp Gln Tyr Ala Lys Ala Val Thr Val Asn Gly Glu Lys Gly
     242               180                 185                 190
     243   Val Val Leu Arg Pro Asp Gln Met Lys Trp Thr Ala Pro Leu Lys Pro
     244               195                 200                 205
     245   Phe Ser His Pro Val Asp Ala Val Ile Tyr Glu Thr His Leu Arg Asp
     246       210                 215                 220
     247   Phe Ser Ile His Glu Asn Ser Gly Met Ile Asn Lys Gly Lys Tyr Leu
     248   225                 230                 235                 240
     249   Ala Leu Thr Glu Thr Asp Thr Gln Thr Ala Asn Gly Ser Ser Ser Gly
     250               245                 250                 255
     251   Leu Ala Tyr Val Lys Glu Leu Gly Val Thr His Val Glu Leu Leu Pro
     252               260                 265                 270
     253   Val Asn Asp Phe Ala Gly Val Asp Glu Glu Lys Pro Leu Asp Ala Tyr
     254               275                 280                 285
     255   Asn Trp Gly Tyr Asn Pro Leu His Phe Phe Ala Pro Glu Gly Ser Tyr
     256       290                 295                 300
     257   Ala Ser Asn Pro His Asp Pro Gln Thr Arg Lys Thr Glu Leu Lys Gln
     258   305                 310                 315                 320
     259   Met Ile Asn Thr Leu His Gln His Gly Leu Arg Val Ile Leu Asp Val
     260               325                 330                 335
```

VERIFICATION SUMMARY   DATE: 02/22/2001
PATENT APPLICATION: US/09/262,126B   TIME: 12:09:02

        Input Set : A:\GC396-2 seq.txt
        Output Set: N:\CRF3\02222001\I262126B.raw

L:34 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:34 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:57 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:67 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:210 M:341 W: (46) "n" or "Xaa" used, for· SEQ ID#:2